## Figure 1A

	1	DIVLTQSPAS	LAVSLGQRAT	MSCRAGESVD	IFGVGFLHWY	QQKPGQPPKL
	51	LIYRASNLES	GIPVRFSGTG	sRTDFTLIID	PVEADDVATY	YCQQTNEDPY
_						
	101	TFGGGTKLEI	KGGGGSGGG	SGGGGSGGG	SGGGGSGGG	SEVQLQQSGA
_						
	151	ELVEPGASVK	LSCTASGFNI	KDTYMHWVKQ	RPEQGLEWIG	RIDPANGNSK
		·	•			•
	201	YVPKFQGKAT	ITADTSSNTA	YLQLTSLTSE	DTAVYYCAPF	GYYVSDYAMA
	251	YWGQGTSVTV	SS			

## Figure 1B

1	GACATCGTCC	TGACCCAGAG	CCCGGCAAGC	CTGGCTGTTT	CCCTGGGCCA
51	GCGTGCCACT	ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
101 .	TCGGTTTTCT	GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC	GCCAAAACTG
151	CTGATCTATC	GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG	TACGTTTCTC
201	CGGTACTGGC	TCTCGTACTG	ATTTTACCCT	GATTATCGAC	CCGGTGGAAG
251	CAGACGATGT	TGCCACCTAC	TATTGCCAGC	AGACCAACGA	GGATCCGTAC
301	ACCTTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
351	TGGTGGTGGT	AGCGGCGGCG	GTGGTAGCGG	TGGCGGTGGC	AGCGGTGGTG
401	GTGGCTCTGG	TGGCGGTGGC	TCTGAAGTGC	AGCTGCAGCA	GTCCGGTGCG
451	GAGCTCGTTG	AACCGGGCGC	TTCTGTGAAA	CTGTCTTGCA	CTGCATCTGG
501	TTTCAACATT	AAGGACACCT	ACATGCACTG	GGTGAAACAA	CGCCCGGAAC
551	AGGGTCTGGA	GTGGATCGGT	CGCATCGATC	CGGCTAACGG	TAACAGCAAA
601	TACGTGCCAA	AATTCCAGGG	TAAAGCAACC	ATCACTGCTG	ATACCTCCTC
651	TAACACTGCT	TACCTGCAGC	TGACTTCCCT	GACTAGCGAA	GACACCGCGG
701	TTTATTACTG	CGCTCCGTTC	GGCTACTATG	TCAGCGATTA	CGCAATGGCC
751	TACTGGGGTC	AGGGCACCTC	TGTTACCGTT	TCTAGC .	

# Figure 1C

263	TPVSEKQL A	EVVANTITP L	MKAQSVPGM A	VAVIYQGKP	
301	HYYTFGKADI	AANKPVTPQT	LFELGSISKT	FTGVLGGDAI	ARGEISLDDA
351	VTRYWPQLTG	KQWQGIRMLD	LATYTAGGLP	LQVPDEVTDN	ASLLRFYQNW
-401	QPQWKPGTTR	LYANASIGLF	GALAVKPSGM	PYEQAMTTRV	LKPLKLDHTW
451	INVPKAEEAH	YAWGYRDGKA	VRVSPGMLDA	QAYGVKTNVQ	MANWVMANM
501	APENVADASL	KQGIALAQSR	YWRIGSMYQG	LGWEMLNWPV	EANTVVETSF
551	GNVALAPLPV	ÄEVNPPAPPV	KASWVHKTGS	TGGFGSYVAF	IPEKQIGIVM
602	LANTSYPNPA	RVEAAYHILE	ALQ		

## Figure 1D

1	ACACCGGTGT	CAGAAAAACA	GCTGGCGGAG	GTGGTCGCGA	ATACGATTAC
51	CCCGCTGATG	AAAGCCCAGT	CTGTTCCAGG	CATGGCGGTG	GCCGTTATTT
101	ATCAGGGAAA	ACCGCACTAT	TACACATTTG	GCAAGGCCGA	TATCGCGGCG
151	AATAAACCCG	TTACGCCTCA	GACCCTGTTC	GAGCTGGGTT	CTATAAGTAA
201	AACCTTCACC	GGCGTTTTAG	GTGGGGATGC	CATTGCTCGC	GGTGAAATTT
251	CGCTGGACGA	TGCGGTGACC	AGATACTGGC	CACAGCTGAC	GGGCAAGCAG
301	TGGCAGGGTA	TTCGTATGCT	GGATCTCGCC	ACCTACACCG	CTGGCGGCCT
351	GCCGCTACAG	GTACCGGATG	AGGTCACGGA	TAACGCCTCC	CTGCTGCGCT
401	TTTATCAAAA	CTGGCAGCCG	CAGTGGAAGC	CTGGCACAAC	GCGTCŢTTAC
451	GCCAACGCCA	GCATCGGTCT	TTTTGGTGCG	CTGGCGGTCA	AACCTTCTGG
501	CATGCCCTAT	GAGCAGGCCA	TGACGACGCG	GGTCCTTAAG	CCGCTCAAGC
551	TGGACCATAC	CTGGATTAAC	GTGCCGAAAG	CGGAAGAGGC	GCATTACGCC
601	TGGGGCTATC	GTGACGGTAA	AGCGGTGCGC	GTTTCGCCGG	GTATGCTGGA
651	TGCACAAGCC	TATGGCGTGA	AAACCAACGT	GCAGGATATG	GCGAACTGGG
701	TCATGGCAAA	CATGGCGCCG	GAGAACGTTG	CTGATGCCTC	ACTTAAGCAG
751	GGCATCGCGC	TGGCGCAGTC	GCGCTACTGG	CGTATCGGGT	CAATGTATCA
801	GGGTCTGGGC	TGGGAGATGC	TCAACTGGCC	CGTGGAGGCC	AACACGGTGG
851	TCGAGACGAG	TTTTGGTAAT	GTAGCACTGG	CGCCGTTGCC	CGTGGCAGAA
901	GTGAATCCAC	CGGCTCCCCC	GGTCAAAGCG	TCCTGGGTCC	ATAAAACGGG
951	CTCTACTGGC	GGGTTTGGCA	GCTACGTGGC	CTTTATTCCT	GAAAAGCAGA
1001	TCGGTATTGT	GATGCTCGCG	AATACAAGCT	ATCCGAACCC	GGCACGCGTT
1051	GAGGCGGCAT	ACCATATCCT .	CGAGGCGCTA	CAG	

### Figure 1E

1_	DIVLTQSPAS	LAVSLGQRAT	MSCRAGESVD	IFGVGFLHWY	QQKPGQPPKL
3					
51	LIYRASNLES	GIPVRFSGTG	SRTDFTLIID	PVEADDVATY	YCQQTNEDPY
				-	
 101	TFGGGTKLEI	KGGGGSGGG	SGGGGSGGGG	SGGGGSGGG	SEVQLQQSGA
 151	ELVEPGASVK	LSCTASGFNI	KDTYMHWVKQ	RPEQGLEWIG	RIDPANGNSK
201	YVPKFQGKAT	ITADTSSNTA	YLQLTSLTSE	DTAVYYCAPF	GYYVSDYAMA
251	YWGQGTSVTV	_SSTPVSEKQL	AEVVANTITP	LMKAQSVPGM	AVAVIYQGKP
301	HŸYTFGKADI	AANKPVTPQT	LFELGSISKT	FTGVLGGDAI	ARGEISLDDA
351		KQWQGIRMLD	8		
401		LYANASIGLF	•		
451	INVPKAEEAH	YAWGYRDGKA	VRVSPGMLDA	QAYGVKTNVQ	DMANWVMANM
501	APENVADASL	KQGIALAQSR	YWRIGSMYQG	LGWEMLNWPV	EANTVVETSF
551	GNVALAPLPV	AEVNPPAPPV	KASWVHKTGS	TGGFGSYVAF	IPEKQIGIVM
601	LANTSYPNPA	RVEAAYHILE	ALQ		

## Figure 1F

	•	•		
1	<del>-</del>	TGACCCAGAG	CCCGGCAAGC	CTGGCTGTTT
CCC	TGGGCCA .	•		
51	GCGTGCCACT	ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC
ATT	TTCGGTG		•	•
		GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC
GCC	AAAACTG			• .
151	CTGATCTATC	GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG
	GTTTCTC		•	
	CGGTACTGGC	TCTCGTACTG	ATTTTACCCT	GATTATCGAC
	GTGGAAG			
251		TGCCACCTAC	TATTGCCAGC	AGACCAACGA
	TCCGTAC	100011001110		
		GCGGTACTAA	ΔΟΨΕΘΔΕΔΨΟ	AAAGGCGGTG
	GTTCTGG	GCGGIACIM	HC100HOI110	
		AGCGGCGGCG	CTCCTACCCC	тессестесс
351		DODDODDA	GIGGINGCGG	19909910
	GGTGGTG	mcccccmccc	TCTGAAGTGC	A CCTCCA CCA
	GTGGCTCTGG	1666661666	ICIGAAGIGC	AGCIGCAGCA
	CGGTGCG	************		
<del>-</del>		AACCGGGCGC	TICIGIGAAA	CIGICIIGCA
	CATCIGG	7 7 CC7 C7 CC	7 C 7 E C C 7 C E C	CCTCTTTCTT
		AAGGACACCT	ACATGCACTG	GGTGAAACAA
	CCGGAAC			
		GTGGATCGGT	CGCATCGATC	CGGCTAACGG
•	CAGCAAA			7 mar amagma
		AATTCCAGGG	TAAAGCAACC	ATCACTGCTG
	CCTCCTC			
		TACCTGCAGC	TGACTTCCCT	GACTAGCGAA
	ACCGCGG	· · · ·		
		CGCTCCGTTC	GGCTACTATG	TCAGCGATTA
	AATGGCC			
,		AGGGCACCTC	TGTTACCGTT	TCTAGCACAC
	<b>IGTCAGA</b>			
<b>~</b> ~ ~	AAAACAGCTG	GCGGAGGTGG	TCGCGAATAC	GATTACCCCG
CTG	ATGAAAG			
		TCCAGGCATG	GCGGTGGCCG	TTATTTATCA
GGG	AAAACCG			
901	CACTATTACA	CATTTGGCAA	GGCCGATATC	GCGGCGAATA
AAC	CCGTTAC			
951	GCCTCAGACC	CTGTTCGAGC	TGGGTTCTAT	AAGTAAAACC
	ACCGGCG			•
1001 .	TTTTAGGTGG	GGATGCCATT	GCTCGCGGTG	AAATTTCGCT
	CGATGCG			
1051	GTGACCAGAT	ACTGGCCACA	GCTGACGGGC	AAGCAGTGGC
AGG	TATTCG '		-	

110	1 TATGCTGGAT	CTCGCCACCT	ACACCGCTGG	CGGCCTGCCG
	CTACAGGTAC	•	•	•
115	1 CGGATGAGGT	CACGGATAAC	GCCTCCCTGC	TGCGCTTTTA
7	CAAAACTGG			
	1 CAGCCGCAGT	GGAAGCCTGG	CACAACGCGT	CTTTACGCCA
I	ACGCCAGCAT			
125	1 CGGTCTTTTT	GGTGCGCTGG	CGGTCAAACC	TTCTGGCATG
	CCTATGAGC		•	
	1 AGGCCATGAC	GACGCGGGTC	CTTAAGCCGC	TCAAGCTGGA
	CCATACCTGG			
	1 ATTAACGTGC	CGAAAGCGGA	AGAGGCGCAT	TACGCCTGGG
	GCTATCGTGA			
	1 CGGTAAAGCG	GTGCGCGTTT	CGCCGGGTAT	GCTGGATGCA
. (	CAAGCCTATG	•		
	1 GCGTGAAAAC	CAACGTGCAG	GATATGGCGA	ACTGGGTCAT
, (	GCAAACATG			
150	_	ACGTTGCTGA	TGCCTCACTT	AAGCAGGGCA
5	rcgcgctggc			
	1 GCAGTCGCGC	TACTGGCGTA	TCGGGTCAAT	GTATCAGGGT
. (	CTGGGCTGGG			
	1 AGATGCTCAA	CTGGCCCGTG	GAGGCCAACA	CGGTGGTCGA
(	GACGAGTTTT			
	1 GGTAATGTAG	CACTGGCGCC	GTTGCCCGTG	GCAGAAGTGA
7	ATCCACCGGC		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	7 7 CCCCCMCM
	1 TCCCCCGGTC	AAAGCGTCCT	GGGTCCATAA	AACGGGCTCT
1	ACTGGCGGGT		************	T CCT CT TCCC
	1 TTGGCAGCTA	CGTGGCCTTT	ATTCCTGAAA	AGCAGAICGG
	PATTGTGATG	~~~~	CD 7 COCCCC7	CCCCMMCACC
-	1 CTCGCGAATA	CAAGCTATCC	GAACCCGGCA	CGCGIIGAGG
	CGGCATACCA			
1.85	1 TATCCTCGAG	GCGCTACAG		

Figure 2A

		15410				
D	IVLTC	SPAS LSVSLG	QRAT MSCRAG	ESVD IFGVGF	LHWY QQKPGQ	PPKL
-	51	LIYRASNLES	GIPVRFSGTG	SGTDFTLIID	PVEADDVATY	YCQQTNEDPY
	101	TFGGGTKLEI	KGGGGSGGG	SGGGGSGGG	SGGGGSGGG	<i>S</i> EVQLQQSGA
	151	ELVEPGASVK	LSCTASGFNI	KDTYMHWVKQ	RPEQGLEWIG	RIDPANGNSK
_	201				DTAVYYCAPF	*
	251	YWGQGTSVTV	,			

## Figure 2B

1	GACATCGTCC	TGACCCAGAG	CCCGGCAAGC	CTGTCTGTTT	CCCTGGGCCA
51	GCGTGCCACT	ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
101	TCGGTTTTCT	GCACTGGTAC		CGGGTCAGCC	
151	CTGATCTATC	GTGCTTCTAA		GGCATCCCGG	TACGTTTCTC
201	CGGTACTGGC		ATTTTACCCT	GATTATCGAC	CCGGTGGAAG
251	CAGACGATGT		TATTGCCAGC	AGACCAACGA	GGATCCGTAC
	ACCTTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
301	TGGTGGTGGT	AGCGGTGGCG		TGGCGGTGGC	
351		TGGCGGTGGC		AGCTGCAGCA	
401	GTGGCTCTGG	AACCGGGCGC		CTGTCTTGCA	
451	GAGCTCGTTG	AACCGGGCGC		GGTGAAACAA	
501	TTTCAACATT			CGGCTAACGG	
551	AGGGTCTGGA	GTGGATCGGT	_		ATACCTCCTC
601		AATTCCAGGG	TAAAGCAACC	GACTAGCGAA	
651	TAACACTGCT				CGCAATGGCC
701		CGCTCCGTTC	GGCTACTATG		CGCMAIGGCC
751	TACTGGGGTC	AGGGCACCTC	TGTTACCGTT	TCTAGC	

#### Figure 3

TPVSEKQL AEVVANTITP LMAAQSVPGM AVAVIYQGKP

301 HYYTFGKADI AANKPVTPQT LFELGSISKT FTGVLGGDAI ARGEISLDDA

351 VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW

401 QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW

451 INVPKAEEAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWVMANM

501 APENVADASL KQGIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF

551 GNVALAPLPV AEVNPPAPPV KASWVHKTGS TGGFGAYVAF IPEKQIGIVM

601 LANTSYPNPA RVEAAYHILE ALQ

## Figure 4A

1	DIVLTQSPAS	LSVSLGQRAT	MSCRAGESVD	IFGVGFLHWY	QQKPGQPPKL
51	LIYRASNLES			PVEADDVATY	
 101	TFGGGTKLEI	KGGGGSGGG	SGGGSGGGG	SGGGSGGG	<u>SEVQLQQSGA</u>
151	ELVEPGASVK	LSCTASGFNI	KDTYMHWVKQ	RPEQGLEWIG	RIDPANGNSK
201	YVPKFQGKAT	ITADTSSNTA	YLQLTSLTSE	DTAVYYCAPF	GYYVSDYAMA
251	YWGQGTSVTV	SSTPVSEKQL	AEVVANTITP	LMKAQSVPGM	AVAVIYQGKP
301	HYYTFGKADI	AANKPVTPQT	LFELGSISKT	FTGVLGGDAI	ARGEISLDDA
351	VTRYWPQLTG	KQWQGIRMLD	LATYTAGGLP	LQVPDEVTDN	ASLLRFYQNW
401	QPQWKPGTTR	LYANASIGLE	GALAVKPSGM	PYEQAMTTRV	LKPLKLDHTW
451	INVPKAEEAH	YAWGYRDGKA	VRVSPGMLDA	QAYGVKTNVQ	DMANWVMANM
501	APENVADASL	KQGIALAQSR	YWRIGSMYQG	LGWEMLNWPV	EANTVVETSF
551	GNVALAPLPV	AEVNPPAPPV	KASWVHKTGS	TGGFGSYVAF	' IPEKQIGIVM
601	LANTSYPNPA	RVEAAYHILE	ALQ		

# Figure 4B

1.	GACATCGTCC	TGACCCAGAG	CCCGGCAAGC	CTGTCTGTTT	CCCTGGGCCA
51	GCGTGCCACT	' ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
101	TCGGTTTTCT	GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC	GCCAAAACTG
151	CTGATCTATC	GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG	TACGTTTCTC
201	CGGTACTGGC	TCTGGTACTG	ATTTTACCCT	GATTATCGAC	CCGGTGGAAG
251	CAGACGATGT	TGCCACCTAC	TATTGCCAGC	AGACCAACGA	GGATCCGTAC
301	ACCTTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
351	TGGTGGTGGT	AGCGGTGGCG	GTGGTAGCGG	TGGCGGTGGC	AGCGGTGGTG
401	GTGGCTCTGG	TGGCGGTGGC	TCTGAAGTGC	AGCTGCAGCA	GTCCGGTGCG
451	- GAGCTCGTTG	AACCGGGCGC	TTCTGTGAAA	CTGTCTTGCA	CTGCATCTGG
501	TTTCAACATT	AAGGACACCT	ACATGCACTG	GGTGAAACAA	CGCCCGGAAC
551	AGGGTCTGGA	GTGGATCGGT	CGCATCGATC	CGGCTAACGG	TAACAGCAAA
601	TACGTGCCAA	AATTCCAGGG	TAAAGCAACC	ATCACTGCTG	ATACCTCCTC
651	TAACACTGCT	TACCTGCAGC	TGACTTCCCT	GACTAGCGAA	GACACCGCGG
701	TTTATTACTG	CGCTCCGTTC	GGCTACTATG	TCAGCGATTA	CGCAATGGCC
751	TACTGGGGTC	AGGGCACCTC	TGTTACCGTT	TCTAGCACAC	CGGTGTCAGA
801	AAAACAGCTG	GCGGAGGTGG	TCGCGAATAC	GATTACCCCG	CTGATGAAAG
851	CCCAGTCTGT	TCCAGGCATG	GCGGTGGCCG		GGGAAAACCG
901	CACTATTACA	CATTTGGCAA	GGCCGATATC		AACCCGTTAC
951	GCCTCAGACC	CTGTTCGAGC	TGGGTTCTAT	AAGTAAAACC	TTCACCGGCG
1001	TTTTAGGTGG	GGATGCCATT	GCTCGCGGTG	AAATTTCGCT	GGACGATGCG
1051	GTGACCAGAT	ACTGGCCACA	GCTGACGGGC	AAGCAGTGGC	AGGGTATTCG
1101	TATGCTGGAT	CTCGCCACCT	ACACCGCTGG		CTACAGGTAC
1151	CGGATGAGGT	CACGGATAAC	GCCTCCCTGC		TCAAAACTGG
1201	CAGCCGCAGT	GGAAGCCTGG	CACAACGCGT		ACGCCAGCAT
1251	CGGTCTTTT	GGTGCGCTGG	CGGTCAAACC		CCCTATGAGC
1301	AGGCCATGAC	GACGCGGGTC	CTTAAGCCGC		CCATACCTGG
1351	ATTAACGTGC	CGAAAGCGGA	AGAGGCGCAT		GCTATCGTGA
1401	-	GTGCGCGTTT	CGCCGGGTAT	GCTGGATGCA	
1451	• •	CAACGTGCAG		ACTGGGTCAT	
1501	• • • • • • • • • • • • • • • • • • • •	ACGTTGCTGA		AAGCAGGGCA	
1551·	GCAGTCGCGC		TCGGGTCAAT	GTATCAGGGT	•
1601	AGATGCTCAA			CGGTGGTCGA	
1651	GGTAATGTAG			GCAGAAGTGA	
1701	TCCCCCGGTC		GGGTCCATAA		ACTGGCGGGT
1751	TTGGCAGCTA		ATTCCTGAAA		TATTGTGATG
1801	CTCGCGAATA TATCCTCGAG		GAACCCGGCA	CGCGTTGAGG	CGGCATACCA
1851	TATCCTCGAG	GCGCTACAG		Ť	

# Figure 4C

1	DIVLTQSPAS	L <b>S</b> VSLGQRAT	MSCRAGESVD	TEGVGETHWY	QQKPGQPPKL
			*		
51	LIYRASNLES	GIPVRFSGTG	S <b>G</b> TDFTLIID	PVEADDVATY	YCQQTNEDPY
 				<u>:</u>	
101	TFGGGTKLEI	KGGGGSGGG	SGGGGSGGG	SGGGSGGG	SEVQLQQSGA
151	ELVEPGASVK	LSCTASGFNI	KDTYMHWVKQ	RPEQGLEWIG	RIDPANGNSK
201	YVPKFQGKAT	ITADTSSNTA	YLQLTSLTSE	DTAVYYCAPF	GYYVSDYAMA
251	YWGQGTSVTV	SSTPVSEKQL	AEVVANTITP	LM <b>A</b> AQSVPGM	AVAVIYQGKP
301	HYYTFGKADI	AANKPVTPQT	LFELGSISKT	FTGVLGGDAI	ARGEISLDDA
351	VTRYWPQLTG	KQWQGIRMLD	LATYTAGGLP	LQVPDEVTDN	ASLLRFYQNW
401	QPQWKPGTTR	LYANASIGLF	GALAVKPSGM	PYEQAMTTRV	LKPLKLDHTW
451	INVPKAEEAH	YAWGYRDGKA	VRVSPGMLDA	QAYGVKTNVQ	DMANWVMANM
501	APENVADASL	KQGIALAQSR	YWRIGSMYQG	LGWEMLNWPV	EANTVVETSF
551	GNVALAPLPV	AEVNPPAPPV	KASWVHKTGS	TGGFGAYVAF	IPEKQIGIVM
601	LANTSYPNPA	RVEAAYHILE	ALQ		

## Figure 4D

1	GACATCGTCC	TGACCCAGAG	CCCGGCAAGC	CTGTCTGTTT	CCCTGGGCCA
51	GCGTGCCACT	ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
101	TCGGTTTTCT	GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC	GCCAAAACTG
151	CTGATCTATC	GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG	TACGTTTCTC
.201	CGGTACTGGC	TCTGGTACTG	ATTTTACCCT	GATTATCGAC	CCGGTGGAAG
251	CAGACGATGT	TGCCACCTAC	TATTGCCAGC	AGACCAACGA	GGATCCGTAC
301	ACCTTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
351	TGGTGGTGGT	AGCGGTGGCG	GTGGTAGCGG	TGGCGGTGGC	AGCGGTGGTG
401	GTGGCTCTGĠ	TGGCGGTGGC	TCTGAAGTGC	AGCTGCAGCA	GTCCGGTGCG
451	GAGCTCGTTG	AACCGGGCGC	TTCTGTGAAA	CTGTCTTGCA	CTGCATCTGG
501	TTTCAACATT	AAGGACACCT	ACATGCACTG	GGTGAAACAA	CGCCCGGAAC
551	AGGGTCTGGA	GTGGATCGGT	CGCATCGATC	CGGCTAACGG	TAACAGCAAA
601	TACGTGCCAA	AATTCCAGGG	TAAAGCAACC	ATCACTGCTG	ATACCTCCTC
651	TAACACTGCT	TACCTGCAGC	TGACTTCCCT	GACTAGCGAA	GACACCGCGG
701	TTTATTACTG	CGCTCCGTTC	GGCTACTATG	TCAGCGATTA	CGCAATGGCC
751	TACTGGGGTC	AGGGCACCTC	TGTTACCGTT	TCTAGCACAC	CGGTGTCAGA
801	AAAACAGCTG	GCGGAGGTGG	TCGCGAATAC	GATTACCCCG	CTGATGGCGG
851	CCCAGTCTGT	TCCAGGCATG	GCGGTGGCCG.		GGGAAAACCG
901	CACTATTACA	CATTTGGCAA	GGCCGATATC	GCGGCGAATA	AACCCGTTAC
951	GCCTCAGACC	CTGTTCGAGC	TGGGTTCTAT	AAGTAAAACC	TTCACCGGCG
1001	TTTTAGGTGG	GGATGCCATT	GCTCGCGGTG	AAATTTCGCT	GGACGATGCG
1051	GTGACCAGAT	ACTGGCCACA	GCTGACGGGC	AAGCAGTGGC	AGGGTATTCG
1101	TATGCTGGAT	CTCGCCACCT	ACACCGCTGG	CGGCCTGCCG	CTACAGGTAC
1151	CGGATGAGGT	CACGGATAAC	GCCTCCCTGC	TGCGCTTTTA	TCAAAACTGG
1201	CAGCCGCAGT	GGAAGCCTGG	CACAACGCGT	CTTTACGCCA	ACGCCAGCAT
1251	CGGTCTTTTT	GGTGCGCTGG	CGGTCAAACC	TTCTGGCATG	CCCTATGAGC
1301	AGGCCATGAC	GACGCGGGTC	CTTAAGCCGC	TCAAGCTGGA	CCATACCTGG
1351	ATTAACGTGC	CGAAAGCGGA	AGAGGCGCAT	TACGCCTGGG	GCTATCGTGA
1401	CGGTAAAGCG	GTGCGCGTTT	CGCCGGGTAT	GCTGGATGCA	CAAGCCTATG
1451	GCGTGAAAAC	CAACGTGCAG	GATATGGCGA	ACTGGGTCAT	GGCAAACATG
1501	GCGCCGGAGA	ACGTTGCTGA	TGCCTCACTT	AAGCAGGGCA	TCGCGCTGGC
1551	GCAGTCGCGC	TACTGGCGTA	TCGGGTCAAT	GTATCAGGGT	CTGGGCTGGG
1601	AGATGCTCAA	CTGGCCCGTG	GAGGCCAACA	CGGTGGTCGA	GACGAGTTTT
1651	GGTAATGTAG	CACTGGCGCC	GTTGCCCGTG	GCAGAAGTGA	ATCCACCGGC
1701	TCCCCCGGTC	AAAGCGTCCT	GGGTCCATAA	AACGGGCTCT	ACTGGCGGGT
1751	TTGGCGCGTA	CGTGGCCTTT	ATTCCTGAAA	AGCAGATCGG	TATTGTGATG
1801	CTCGCGAATA	CAAGCTATCC	GAACCCGGCA	CGCGTTGAGG	CGGCATACCA
1851	TATCCTCGAG	GCGCTACAG			

## Figure 4E

	1 AGGAATTATC CTGGTCTGCT	ATATGAAATA	CCTGCTGCCG	ACCGCTGCTG
	51 GCTCCTCGCT ACCCAGAGCC	GCCCAGCCGG	CCATGGCCGA	CATCGTCCTG
	101 CGGCAAGCCT GTCCTGCAGA	GTCTGTTTCC	CTGGGCCAGC	GTGCCACTAT
	151 GCGGGTGAGT ACTGGTACCA	CTGTTGACAT	TTTCGGTGTC	GGTTTTCTGC
	201 ACAGAAACCG GCTTCTAACC	GGTCAGCCGC	CAAAACTGCT	GATCTATCGT
•	251 TGGAGTCCGG TGGTACTGAT	CATCCCGGTA	CGTTTCTCCG	GTACTGGCTC
	301 TTTACCCTGA CCACCTACTA	TTATCGACCC	GGTGGAAGCA	GACGATGTTG
,	351 TTGCCAGCAG GGTÄCTAAAC	ACCAACGAGG	ATCCGTACAC	CTTCGGTGGC
	401 TGGAGATCAA CGGTGGCGGT	AGGCGGTGGT	GGTTCTGGTG	GTGGTGGTAG
	451 GGTAGCGGTG GCGGTGGCTC	GCGGTGGCAG	CGGTGGTGGT	GGCTCTGGTG
	501 TGAAGTGCAG CCGGGCGCTT	CTGCAGCAGT	CCGGTGCGGA	GCTCGTTGAA
	551 CTGTGAAACT GGACACCTAC	GTCTTGCACT	GCATCTGGTT	TCAACATTAA
	601 ATGCACTGGG GGATCGGTCG	TGAAACAACG	CCCGGAACAG	GGTCTGGAGT
	651 CATCGATCCG	GCTAACGGTA	ACAGCAAATA	CGTGCCAAAA
	701 AAGCAACCAT CCTGCAGCTG	CACTGCTGAT	ACCTCCTCTA	ACACTGCTTA
	751 ACTTCCCTGA CTCCGTTCGG	CTAGCGAAGA	CACCGCGGTT	TATTACTGCG
	801 CTACTATGTC GGCACCTCTG	AGCGATTACG	CAATGGCCTA	CTGGGGTCAG
	851 TTACCGTTTC GGAGGTGGTC			
	901 GCGAATACGA CAGGCATGGC	TTACCCCGCT	GATGGCGGCC	CAGTCTGTTC
	951 GGTGGCCGTT TTTGGCAAGG	ATTTATCAGG	GAAAACCGCA	CTATTACACA
	1001 CCGATATCGC GTTCGAGCTG	GGCGAATAAA	CCCGTTACGC	CTCAGACCCT

1051	GGTTCTATAA CCATTGC	GTAAAACCTT	CACCGGCGTT	TTAGGTGGGG
	TCGCGGTGAA	л <b>т</b> ттссстсс	ACCATCCCCT	GACCAGATAC
	CCACAGC		•	
1151	TGACGGGCAA	GCAGTGGCAG	GGTATTCGTA	TGCTGGATCT
CGC	CCACCTAC			•
1201		GCCTGCCGCT	ACAGGTACCG	GATGAGGTCA
	FATAACGC			• .
- 0 - 1	CTCCCTGCTG	CCCMMMMAMC	N N N N CTCCCN	CCCCCACTCC
		CGCITTIATC	AAAACIGGCA	GCCGCAGIGG
	CCTGGCA			
	CAACGCGTCT	TTACGCCAAC	GCCAGCATCG	GTCTTTTTGG
TGC	CGCTGGCG		·	
1351	GTCAAACCTT	CTGGCATGCC	CTATGAGCAG	GCCATGACGA
CGC	CGGGTCCT	•	•	•
	TAAGCCGCTC	AAGCTGGACC	ATACCTGGAT	TAACGTGCCG
	AGCGGAAG			;
1/51	AGGCGCATTA	CGCCTGGGGC	TATCGTGACG	GTAAAGCGGT
	GCGTTTCG			
	CCCCMVMCC	TGGATGCACA	ACCCTATCCC	CTCAAAACCA
1501		1 GGWI GĊWCW	AGCCIAIGGC	G1G1HHH10G11
	GTGCAGGA		~~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	CCCCCACAAC
1551	_	TGGGTCATGG	CAAACATGGC	GCCGGAGAAC
GT?	rgctgatg			
	CCTCACTTAA	GCAGGGCATC	GCGCTGGCGC	AGTCGCGCTA
	GCGTATC			
1651	GGGTCAATGT	ATCAGGGTCT	GGGCTGGGAG	ATGCTCAACT
GG	CCCGTGGA	: ,		
1701	GGCCAACACG	GTGGTCGAGA	CGAGTTTTGG	TAATGTAGCA
	GCGCCGT			•
	TGCCCGTGGC	AGAAGTGAAT	CCACCGGCTC	CCCCGGTCAA
	CGTCCTGG			
1001	GTCCATAAAA	CGGGCTCTAC	TGGCGGGTTT	. GGCGCGTACG
	CCTTTAT	00000101110		
		CAGATCGGTA	$\Psi$	ССССАВТАСА
1851		CAGAICGGIA	1101041001	000011111011
AGC	CTATCCGA		COMMACONMA	mccmcca.ccc
	ACCCGGCACG	CGTTGAGGCG	GCATACCATA	TCCTCGAGGC
GC1	TACAGTAG			
	GAATTCGAGC	TCCGTCGACA	AGCTTGCGGC	CGCACTCGAG
ATC	CAAACGGG			
2001	CTAGCCAGCC	AGAACTCGCC	CCGGAAGACC	CCGAGGATGT
CGF	AGCACCAC		•	•
2051	CACCACCACC	ACTGAGATCC	GGCTGCTAAC	AAAGCCCGAA
	BAAGCTGA			•
2101	GTTGGCTGCT	GCCACCGCTG	AGCAATAACT	AGCATAACCC
	GGGGCCT			
CTT	CTAAACGGGT	CTTCACCCCT	<b>ՊԻՐԻՐԻՐՐԻՐ</b> Հ	AAGGAGGAAC
		CIIGUGGGI	TITITGCIGN	11100110011110
TAT	ATCCGGA			

		•		
	TTGGCGAATG	GGACGCGCCC	TGTAGCGGCG	CATTAAGCGC
	CGGGTGTG			
	GTGGTTACGC GCGCCCGC	GCAGCGTGAC	CGCTACACTT	GCCAGCGCCC
2301	TCCTTTCGCT	TTCTTCCCTT	CCTTTCTCGC	CACGTTCGCC
GG	CTTTCCCC			
2351 TA	GTCAAGCTCT GTGCTTTA	AAATCGGGGG	CTCCCTTTAG	GGTTCCGATT
	CGGCACCTCG	ACCCCAAAAA	ACTTGATTAG	GGTGATGGTT
	CGTAGTGG	110000111111		
		mcamacaccc	mmmmmccccc	mmmca commo
	GCCATCGCCC	TGATAGACGG	TITITOGCCC	TITGACGITG
	GTCCACGT			
2501	TCTTTAATAG	TGGACTCTTG	TTCCAAACTG	GAACAACACT
CA	ACCCTATC	•		
2551	TCGGTCTATT	CTTTTGATTT	ATAAGGGATT	TTGCCGATTT
	GCCTATTG			•
	GTTAAAAAAT	GAGCTGATTT	AACAAAAATT	TAACGCGAAT
	TAACAAAA	ONOCIONITI	1110111111111	1111000011111
			TGATGCGGTA	mmmmcmccmm
2651	TATTAACGCT	TACAATTTCC	TGATGCGGTA	TTTTCTCCTT
	GCATCTGT			
2701	GCGGTATTTC	ACACCGCATA	TGGTGCACTC	TCAGTACAAT
CT	GCTCTGAT			
2751	GCCGCATAGT	TAAGCCAGCC	CCGACACCCG	CCAACACCCG
CT	GACGCGCC			
	CTGACGGGCT	TGTCTGCTCC	CGGCATCCGC	TTACAGACAA
	TGTGACCG		• • • • • • • • • • • • • • • • • • • •	
0051	TCTCCGGGAG	CTCCATCTCT	$C\Delta C\Delta CCTTTT$	СДСССТСДТС
		CIGCAIGIGI	CAGAGGIIII	CACCUICAIC
	CGAAACGC		~~ ~~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	
	GCGAGACGAA	AGGGCCTCGT	GATACGCCTA	TTTTTATAGG
	AATGTCAT	•		
2951	GATAATAATG	GTTTCTTAGA	CGTCAGGTGG	CACTTTTCGG
GG.	AAATGTGC			
3001	GCGGAACCCC	TATTTGTTTA	TTTTTCTAAA	TACATTCAAA
	TGTATCCG			
	CTCATGAGAC	ΔΔͲΔΔϹϹϹͲϾ	TEGERAGEATE	ACCCGACGCA
	TTGCGCCG	·		
CT	TTGCGCCG	momon occana		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
	AATAAATACC	TGTGACGGAA	GATCACTTCG	CAGAATAAAT
	ATCCTGGT		•	
3151	GTCCCTGTTG	ATACCGGGAA	GCCCTGGGCC	AACTTTTGGC
	AAATGAGA	•		
3201	CGTTGATCGG	CACGTAAGAG	GTTCCAACTT	TCACCATAAT
	AATAAGAT			
	CACTACCGGG	CC T ∆ T T T T T T T T T T T T T T T T T	САСТТАТССА	GATTTTCACG
		COTUTATA	CICILITION	
	CTAAGGAA	71 C 71 T		N C C N C C C C C C C C C C C C C C C C
	GCTAAAATGG	AGAAAAAAT	CACTGGATAT	ACCACCGTTG
AT	ATATCCCA			

				·
	ATGGCATCGT	AAAGAACATT	TTGAGGCATT	TCAGTCAGTT
GC'	<b>ICAATGTA</b>		•	
3401	CCTATAACCA	GACCGTTCAG	CTGGATATTA	CGGCCTTTTT
AA	AGACCGTA			
	AAGAAAATA	AGCACAAGTT	TTATCCGGCC	TTTATTCACA
	CTTGCCCG	1100110111011	11111000000	
		CCMC7.MCCCC	**************************************	CCCAAMCAAA
	CCTGATGAAT	GCTCATCCGG	AATTCCGTAT	GGCAATGAAA
	CGGTGAGC	<i>i</i>		•
3551	TGGTGATATG	GGATAGTGTT	CACCCTTGTT	ACACCGTTTT
CC	ATGAGCAA			
3601	ACTGAAACGT	TTTCATCGCT	CTGGAGTGAA	TACCACGACG
	TTCCGGCA			
AT	GTTTCTACAC	7 H 7 H 7 H H C C C	7 7 C 7 TC TC C C C	CTCTTACCCT
		AIAIAIICGC	AAGAIGIGGC	GIGIIACGGI
GA.	AAACCTGG		·	
	CCTATTTCCC	TAAAGGGTTT	ATTGAGAATA	TGTTTTTCGT
CT	CAGCCAAT			
3751	CCCTGGGTGA	GTTTCACCAG	TTTTGATTTA	AACGTGGCCA
	ATGGACAA	•		
3801	CTTCTTCGCC	ССССТТТТСА	CGATGGGCAA	ATATTATACG
	AGGCGACA	00001111011		
		COCCOMCCCC	7 MMC7 CCMMC	<b>умсумсссст</b>
	AGGTGCTGAT	GCCGCTGGCG	ATTCAGGITC	ATCATGCCGT
CT	GTGATGGC ·			
3901	TTCCATGTCG	GCAGAATGCT	TAATGAATTA	CAACAGTACT
GC	GATGAGTG			
3951	GCAGGGCGGG	GCGTAAAGAC	AGATCGCTGA	GATAGGTGCC
	ACTGATTA			
4001	AGCATTGGTA	ACTGTCAGAC	CAAGTTTACT	CATATATACT
	AGATTGAT			•
114	TTAAAACTTC	v መመመመመ <i>ካ</i> v <b>መ</b> መ	TANACCATC	тасетеааса
		WITTINGIT	THIMMOUTTO	1110010111011
TC	CTTTTTGA			
	TAATCTCATG	ACCAAAATCC	CTTAACGTGA	GTTTTCGTTC
	CTGAGCGT	•	_	
4151	CAGACCCCGT	AGAAAAGATC	AAAGGATCTT	CTTGAGATCC
TT'	<b>PTTTTCTG</b>			•
4201	CGCGTAATCT	GCTGCTTGCA	AACAAAAAA	CCACCGCTAC
	CGGTGGT			••
40E1	TTGTTTGCCG	GATCAAGAGC	TACCAACTCT	TTTTCCGAAG
	AACTGGCT	0111 0111,101100	2	
GTA	AACIGGCI	~~~~~~~~~~~~	7. 7. M 7. CM CM M C	· സസ്
	TCAGCAGAGC	GCAGATACCA	AATACIGITC	IICIAGIGIA
GC(	CGTAGTTA			
	GGCCACCACT	TCAAGAACTC	TGTAGCACCG	CCTACATACC
TC	GCTCTGCT			•
4401	AATCCTGTTA	CCAGTGGCTG	CTGCCAGTGG	CGATAAGTCG
	CTTACCG			
10.	GGTTGGACTC	DAGACGATAC	TTACCGGATA	AGGCGCAGCG
GTC	CGGGCTGA			2.

	4501	ACGGGGGGTT	CGTGCACACA	GCCCAGCTTG	GAGCGAACGA
	CCI	ACACCGA			
		ACTGAGATAC	CTACAGCGTG	AGCTATGAGA	AAGCGCCACG
	CTI	CCCGAAG		•	
	4601	GGAGAAAGGC	GGACAGGTAT	CCGGTAAGCG	GCAGGGTCGG
	AAC	CAGGAGAG			
		CGCACGAGGG	AGCTTCCAGG	GGGAAACGCC	TGGTATCTTT
	ATI	GTCCTGT			
	4701	CGGGTTTCGC	CACCTCTGAC	TTGAGCGTCG	ATTTTTGTGA
	TGO	CTCGTCAG			
		GGGGGCGAG	CCTATGGAAA	AACGCCAGCA	ACGCGGCCTT
	$\mathbf{TT}$	TACGGTTC			
		CTGGCCTTTT	GCTGGCCTTT	TGCTCACATG	TTCTTTCCTG
	CG:	TATCCCC			
		TGATTCTGTG	GATAACCGTA	TTACCGCCTT	TGAGTGAGCT
	GA:	PACCGCTC			~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~
	4901	=	AACGACCGAG	CGCAGCGAGT	CAGTGAGCGA
	GG	AAGCGGAA		000m0m0000	CCCCCMMCCC
		GAGCGCCCAA	TACGCAAACC	GCCTCTCCCC	GCGCGTTGGC
	. CG	ATTCATTA		mmacaca amc	C777CCCCCC
	5001	<del>-</del> · · · · · · · · · · · · · · · · ·	CACGACAGGT	TTCCCGACTG	.GAAAGCGGGC
	AG'	rgagcgca			» CCC» CCCC»
		ACGCAATTAA CTTTACAC	TGTGAGTTAG	CTCACTCATT	AGGCACCCCA
	_	TTTACAC	CCCCTCCTT TO	C $T$	ATTGTGAGCG
	5101	TTTATGCTTC	CGGCTCGTAT	GIIGIGIGGA	ATIGIOAGCO
	GA.	TCACACAGGA	<u>አአርአርርጥአጥር</u>	а <i>с</i> сатсатта	CGCCAAGCTA
•			WUCWGCIWIG	MOONIONIE	000011100111
	TT:	TAGGTGAC		mama camma a	CC
	5201	ACTATAGAAT	ACTCAAGCTT	TCTAGATTAA	GG

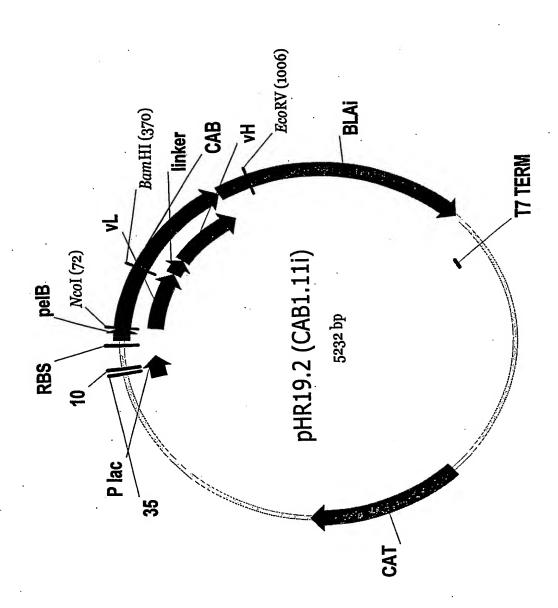
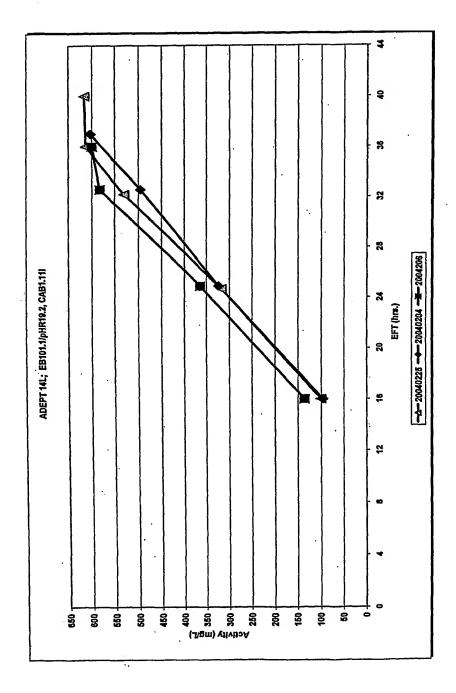


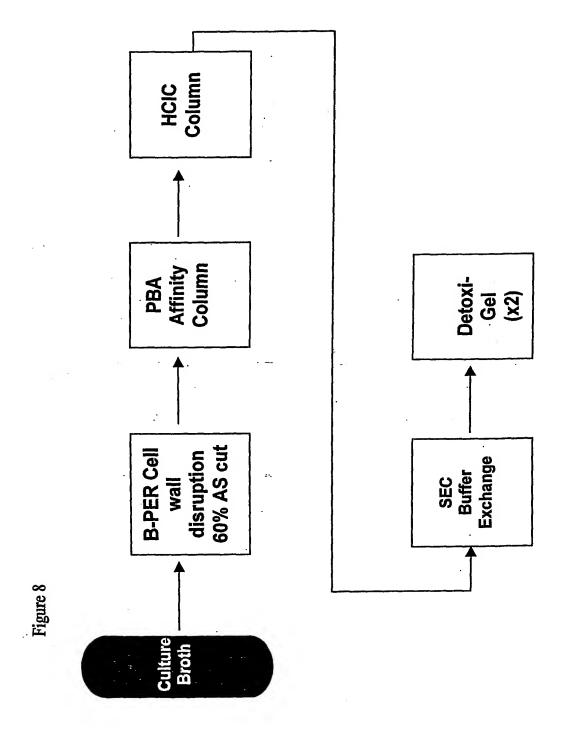
Figure 5

barent CAB1.10 HB14.14 HR14.13 Clone number HR14.10 HR14.9 4F14.8 က sbecitic binding (%)

Figure 6

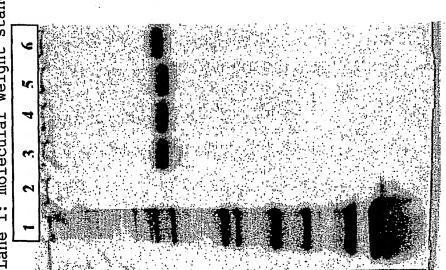


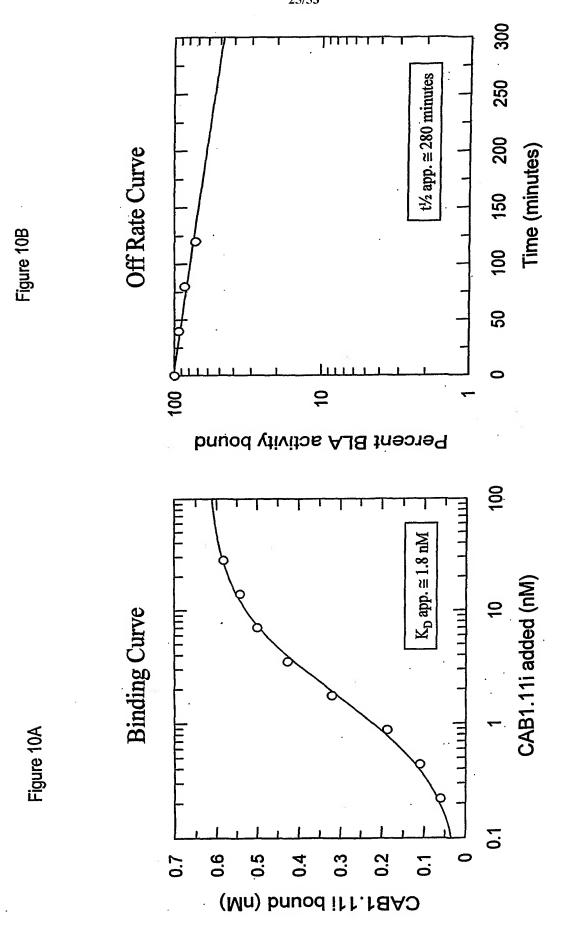


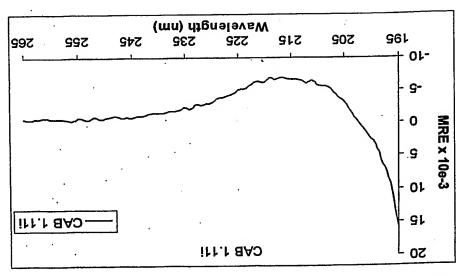


PCT/US2005/012270

Lane 1: molecular weight standard; Lanes 3-5: unrelated proteins; lane 6: CAB1.11i. Figure 9







II əmgia

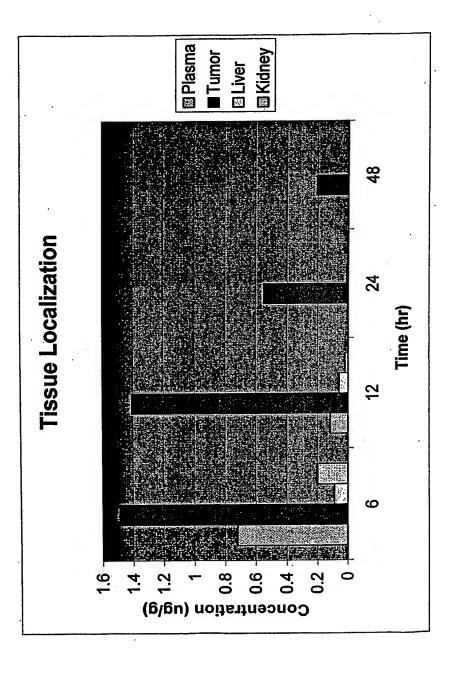


Figure 12

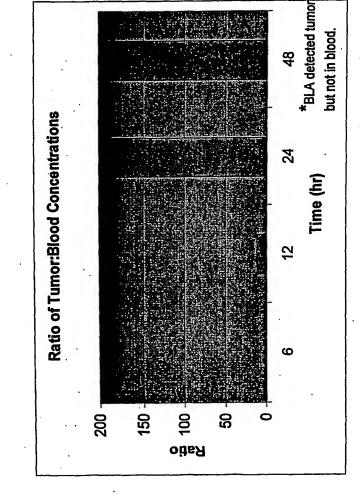
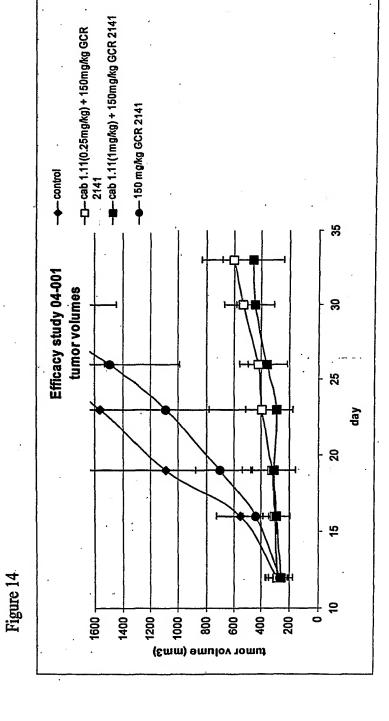


Figure 1



(case)	ASM.	Sample 19. See	Sample Ratiology 4 100 124 12 12 12 12 12 12 12 12 12 12 12 12 12
<u>CI0000000255</u>	DF5	FR00005C7B	Adenocarcinoma of lung
GI0000005496	E	ER5B337147	Adenosaremoma of lung
<u>CI0000011577</u>	FF1	FR5B34059F	Adenocarcinoma of lung
G17000000024f	AF4	FREODESA78	Adenocartinoma telitor a
Cl0000007518	AF5	FR0001FD15	Carcinoma of lung, squamous cell
<u>epecoc6475</u>	4	FR65EE0784	Adenocaromama of colon, meta <b>stallo</b>
<u>Cl0000015252</u>	FF2	FR5B342166	Adenocarcinoma of colon

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F/5088

	i rissue o rongini sire o azindire e e e	#######		
Case Diagnosis  Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	4X	20X	Antial Immunoger
Adenocarcinoma of lung Grade: AJCC G3=Poorly differentiated Stagat NIB are as	Eung/Lung			
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated			<u>26×</u>	
Stage: IIIA	Lung/Lung	<u>4X</u>	<u>20X</u>	
Grade: AJEC G2 Moderately differentiated Siage: IIIA	hing/Elite	4	<u>201</u>	
Carcinoma of lung, squamous cell Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	<u>4X</u>	<u>20X</u>	
Adenocarcinome of colon, metastalic Grade: Not Reported Stage: NV	Colon/Ewee			
Adenocarcinoma of colon			2 <u>08</u>	
Grade: AJCC G3: Poorly differentiated Stage: IIIB	Cecum/Cecum	4X	<u>20X</u>	

FIG. 15-12

lumam Cytokeratin AE1/AE3	CAB/GCR37.08 (0:2ug/ml) Immunogencity: Tumor(100%, Variable to 3+ Cyto)	Immunogencity: Turnor(1) Mixed inflammatory cel
ncity: Tumor(100%, Variable to 3+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High	Mixed inflammatory cells(Variable to 1+ Cyto) Specificity: High  4x 20x	Necrosis(Varia Specifici
<u>20x</u> <u>SF00029758</u>	<u>SF00029756</u>	<u>SF000</u>
	Immunogenoty Tumorids%, Variable to 3+ Cyto Intra-alveotar macrophages (Variable to 2+ Cyto). Mixed infaminatory collst Variable to 3+ Cyto). Specificity: High. 4x 2 26y (Variable to 3+ Cyto).	Immunosencile Turrent Intra alveda marroen a Micerinjanmates vice Spenie T
	Immunogencity: Tumor(100%, 2+ Cyto) Cellular stroma(1+ Cyto)	Immunogencity: Tur Cellular stroi
	Chronic inflammatory cells(Variable to 1+ Cyto) Specificity: High	Chronic inflammatory of Specifici
	<u>4x</u> <u>20x</u>	<u>4x</u>
	<u>SF0002977F</u>	<u>SF000</u>
	Immunoceuchy Tumor(75%, Variable to 4± Cyto) Cellular Suromar(Variable to 2±89%) Necres (Sy arable to 2±89%) Intra avecta macrophaces (Variable to 2±80%) Specifiedly Hintly 4x 5560029788	tomunocencio Tunga Cellular Stronga Se resparva Intra-alvena macrosoci Spenari 12
	Immunogencity: Tumor(100%, 3+ Cyto)	immunogencity: Tur
-	Fibrotic stroma(1+ Cyto)  Necrosis(Variable to 3+ EC)  Specificity: High	Fibrotic stror Necrosis(Varia Specifici
	<u>4x</u> <u>20x</u>	<u>4×</u>
	<u>SF0002975F</u>	<u>SF000</u>
ogancty: Humar(95%, Variable to 34;  Mem Variable to 3+ Cyto)  rolle storia(Variable to 3+ Cyto)  mail liver parenchyma(2+1, Xto)  Necrosis(Variable to 6+ Eq.)  Specificity: High 1 = 1.  20x  SEROO297644	Immunosenary Tumort95% Variable to 3 *  Mem Variable to 3 * Cytothic 2 *  Ebroile Stromary anable to 1 * Gyto) *  Namar liver pare covinat 1 * Cyto *  Necrosis (variable to 3 * EC) *  Specificity High:  4 *  **SE00029768***  Journal liver parenchyma shows positive staining (1*)	Implingenalte The S. Mentivarian Ebroile stories to the Lornal Luci Section Neurosis (V. Section Sec
	(mmunogencity: Tumor(65%, Variable to 3+ Mem,Variable to 3+ Cyto)	immunogencity: Tumc Mem,Variabli
· 1	Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ Cyto)	Cellular stroi Normal muscle(Va
ļ	Specificity: High  4x  20x	Specifici
1	<u>SF00029783</u>	<u>SF000</u>

F16. 16- 0

(v. (0.20g/ml)	GAB/EGR5798 (02200/ml)	CAB/GCR8886 (0:49.60g)
00%, Variable to 3+ Cyto) Ils(Variable to 3+ Cyto) able to 2+ EC) ity: High 20x 29757	immunogencity: Tumor(100%, Variable to 3+ Cyto) Mixed inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x SF00029753	Immunogencity: Tumor(100%, Variable Mixed Inflammatory cells(Variable to Specificity: High 4x 20x SF00029754
Wig Vanable to 31 (709) pas(Vanable to 21 (709) listVanable to 21 (709) listVanable to 21 (700) lig High  20x 29.756	mmenegenciy Tumori 10%, Vanahle to 2+0 (to)? Intra-alveolar macrophages (Variable to 2+0 (to)? Mixed inflammatory cells (Variable to 2+0 (to)?  Specificity High  AX  SF60029759	mmunogench/, TumortUV, Varian Inita alveolar macrophages (Variation Mixedinilarity atorygels (Variation Specificity, High 4x 20 5E6002975A
mor(100%, 2+ Cyto) ma(1+ Cyto) ells(Variable to 1+ Cyto) ity: High 20x	Immunogendty: Tumor(100%, 2+ Cyto) Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x SF0002977D	immunogencity: Tumor(100%, 2+ Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to Specificity: High 4x 20x SF0002977E
ESTANDA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMP	Immuneeanth Tumor (45%) Variable to 4+ Gylor. Gelfular Stroma (Variable to 5+ Sylor. Necrosis (Variable to 5+ Sylor. Intra-al yeolar macrophages (Variable in 5+ Sylor. Specificity Fright 4X 1 4 5 SEG0029789	mounterentiv Filmet (2001) anals Callular Stromet (analog is 1000) analog is 1000 (2000)
Tior(100%, 3+ Cyto) ma(1+ Cyto) able to 3+ EC) ity: High 20x 129760	Immunogencity: Tumor(100%, 3+ Cyto) Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x SF0002975D	Immunogencity: Tumor(100%, 3+ Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x SF0002975E
r (38%; Variable to sit, we see the St. We see the	himunogencipia jurio (95% variable to the Mem Veniable to 3 % violethe in Mem Veniable to 3 % violethe in Fibroite stromat (Variable to 5 % violethe in Normali (esparenchymat (1 % violethe in Normali (espar	Immunotiench Turnutis  21
x(85%, Variable to 3+ e to 3+ Cyto) ma(1+ Cyto) ariable to 2+ Cyto) ity: High 20x	Immunogencity: Tumor(95%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029781	Immunogencity: Tumor(95%, Variab Mem,Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ C Specificity: High 4x SF00029782
-	15-D	

34/53	3

iill	New Missell Control (Section 2018)
to 3+ Cyto) 1+ Cyto)	Immunogencity: N/A Specificity: Unknown
	<u>SF00029755</u>
to 2+ Cyte) 12+ Cyte) 2+ Cyte)	
Cyto)	
1+ Cyto)	
io 3 + Cyto) Yeo) 12 + Cyto) Y 2 Cyto)	
le to 31 vie) no) taining (1+)	imnurogenciy: NA Specificity Unknown;  SEBBUSTES
He to 3+	
· ·	FIG 15E

<u>@10000017870</u>	961	FR65EE7B3D	Adenocarcinoma of eolon
<u>C10000010013</u>	AF2	FR00028F2E	Adenocarcinoma of pancreas, metastatic
<u>@10000009651</u>	Æ	FR0002 <b>51.11</b>	Adenocaronoma of pancreas, buctal
<u>C10000008690</u>	CF4	FR00027B0E	Adenocarcinoma of pancreas, ductal
<u>@l0000007678</u>	AF3	FR0002575B	Adenocarcinoma of pancreas, duotal
<u>C10000009736</u>	AF2	FR0002BAB4	Adenocarcinoma of pancreas, ductal

FIG. 15-F

	, ,		٠,	
Adenocarcinoma of colon Grade: AJCC G2: Moderately differentiated Stage: IIIC	Colon/Colon	XXXXX	26X	
Adenocarcinoma of pancreas, metastatic Grade: Not Reported Stage: IV	Pancreas/Omentum	<u>4X</u>	<u>20X</u>	Immu Fibros
Adenocarcinome of pancreas, ductal Grade: AJGC G2 Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>ax</u>	20X	
Adenocarcinoma of pancreas, ductal Grade: AJCC G1: Well differentiated Stage: IIA	Pancreas/Pancreas	<u>4X</u>	20X	
Adenocarcinoma of pencreas ductal grade: AJCC G2: Moderately differentiated Stage: III	Pancreas/Pancreas			
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>4X</u>	<u>20X</u>	

FIG.
15-G

	immunogendty: Turnor(100%, 3+ Cyte) Gellular stroma(1+ Cyta) Necrosis (Vanable te 3+ EG) Specificity: High  203 SEC0029787	Immunogenetke Tur Cellulanstrie NecrosiscVärk Specific 44 SF-080
inogencity: Tumor(100%, 3+ Cyto) adipose tissue(Variable to 1+ Cyto) Specificity: High 20x SF0002977C	Immunogencity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High 4x 20x SF0002977A	Immunogencity: Tur Fibroadipose tissue( Specifici 4x SF000.
	Immunogenchy Tumorci (190%; 4+ Cyto) Desmoplastic stroma (Variable te 2+ Cyto) Specificity: Highi: 4x 29x : 5F00629771	immunogencity. Tur Desmoplastic strope Special 4x
	Immunogendty: Tumor(100%, 3+ Cyto) Myxold stroma(Variable to 2+ Cyto) Specificity: High 4x 20x SF0002976D	Immunogencity: Tur Myxold stroma(Va Specifici 4x SF000.
	Immunogencity Tumor(85%: Variable to 3+ 9yte)  Cellular shome(Variable to 1+ 6yte)  Chronic pencrealitis(Variable to 1+ 6yte)  Specificity: High  20x  SF00029763	Immunogencity: Turnisms Sellular stroma in Chinonic pancre artist Spenific  11 SF-040
	Immunogencity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 2+ Cyto) Fibrotic stroma(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029775	Immunogencity: Tur Chronic pancreatitis( Fibrotic stroma(Vz Specifici 4x

FIG

15-H

nor(480%; 8+ Cyto) ma(1+ Cyto) able to 3+ EG! ity: High 20x 29788	immunogencity Tumor(100%, 3+ 6yte) Cellular stroma(1+ 6yte) Necresis (Variable to 3+ E.G.) Specificity, High: 4x 20x SF00029785	Immunogencity: Tumor(300%; 84 Cellular stroma(1): Cyrial Necrosis(Variable to 3): E41 Specificity: Flight; 208 SF00029786
mor(100%, 3+ Cyto) (Variable to 2+ Cyto) ity: High 20x 2977B	Immunogencity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029777	Immunogencity: Tumor(100%, 3+ Fibroadipose tissue(Variable to 2+ Specificity: High 4x 20x SF00029778
nor(100%; 6+ Cylo) (Vanable to 2+ Cylo) (by High 20x 29772	Immunogencity/Tumor(100%; 31 Cylb). Desmoplastic stromat/variable to 21 Cylc). Specificity: High:  20x SF00029770	Iremunogencity; Tumor (100%, 8) Desmoplastic stromacy anable to 4 specificity; High.  4x SF0002976F
mor(100%, 3+ Cyto) iriable to 2+ Cyto) ity: High 20x 2976E	Immunogencity: Tumor(100%, 3+ Cyto) Myxold stroma(Variable to 2+ Cyto) Specificity: High 4x 20x SF0002976B	immunogencity: Tumor(100%, 3+ Myxoid stroma(Variable to 2+ C) Specificity: High 4x 20x SF0002976C
is% Yanabie to 3+ Gwols anabie to 1+ Cyto) Wahabie to 1+ Cyto) 1 - lly High 20x 29764	Immunosenaly; Tumor(85%; Vanable to #F Eylo)  Callular stoma (Vanable to #F Cylo)  Chronic panera attis (Vanable to F Cylo)  Specificity; High  4x  20x  SF60029761	Immunogenchy Tunior 65% Vaniabe. Cellular stroma (Vaniable to she she chronic pancreallus (Vaniable tell) Specificity High  4x 20x  SF00029162
mor(100%, 3+ Cyto) (Variable to 2+ Cyto) ariable to 2+ Cyto) ity: High 20x	Immunogencity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Specificity: High  4x  20x  SF00029773	immunogencity: Tumor(100%, 3+ Chronic pancreatitis(Variable to 2+ Fibrotic stroma(Variable to 2+ C Specificity: High  4x 20x  SF00029774

F16.
15- I

	Cyto)	
	Cyto)	Immunogencity: N/A Specificity: N/A
		<u>SF00029779</u>
FIG.	Gyte) Gylu)	
FIG.	Cyto) yto)	
	ic 5+ Cyin) Mey Cyun	
	Cyto) Cyto) yto)	

Eliminated From Plasma and Retained in Tumor to At 10 bil CAB 1.11.

### Least 96 hr

Plasma and tumor GCR-8886 concentration-time profiles (log-linear scale)

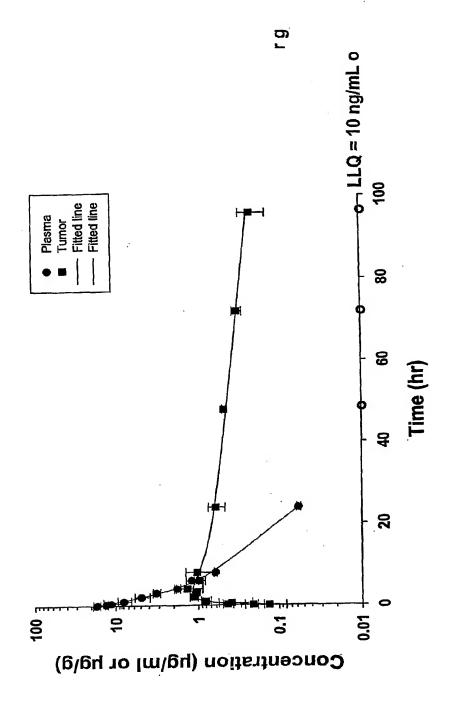
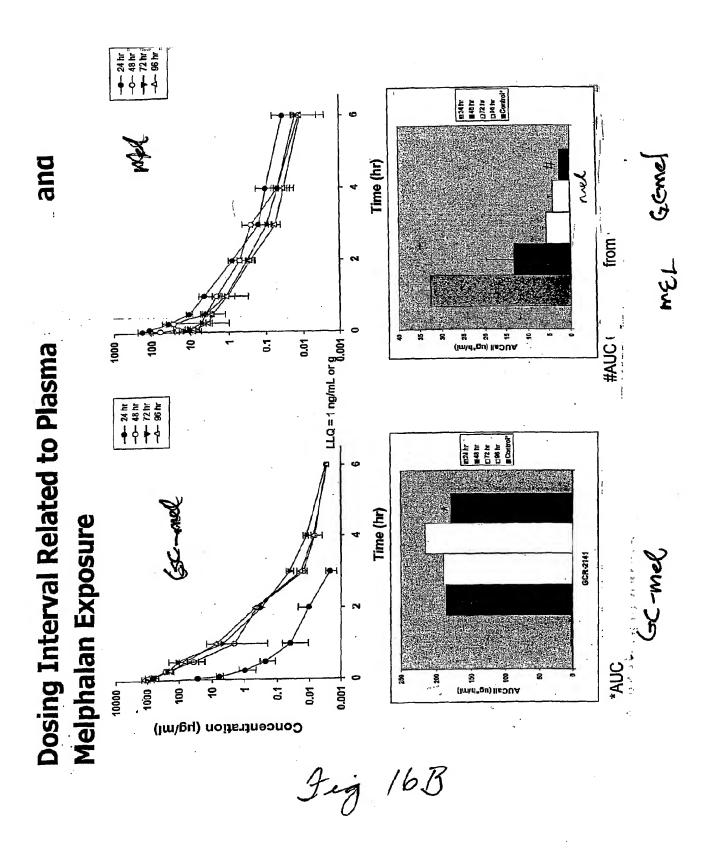
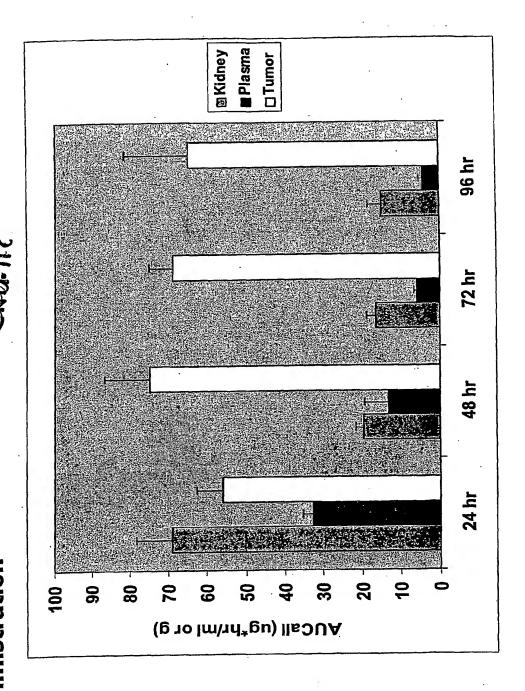


Fig 16A

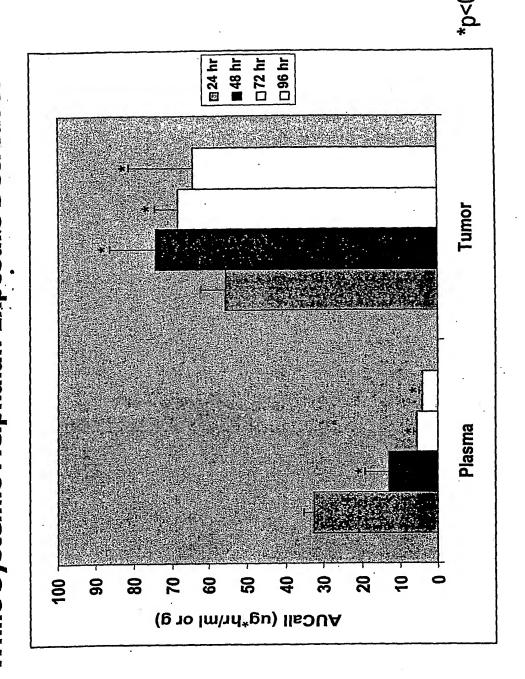


is Decreased with and GCR Increased Interval Between GCR-Plasma and Kidney Exposure to **Administration** 



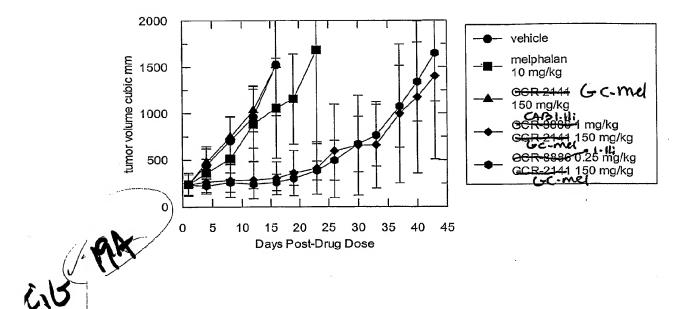
3 mg 17

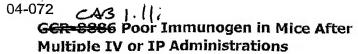
### Efficacious Tumor Melphalan Exposures Achieved at Each Time Interval While Systemic Melphalan Exposure Decreased

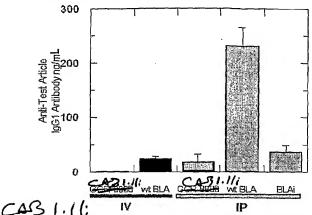


Efficacy demonstrated at 24 hr interval in TLS174T xenograft mouse

model





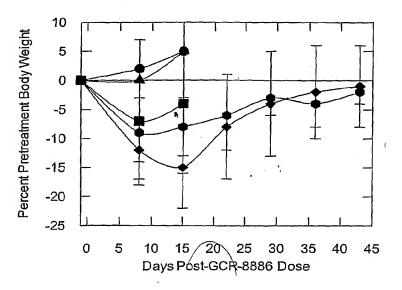


\*GCR-8886 weakly immunogenic after multiple IP doses in alum- similar to BLAi

Confidential

Fi 6 20

### 04-066 completed



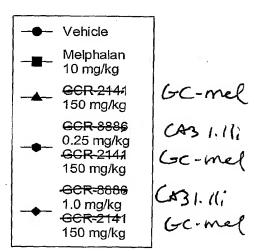
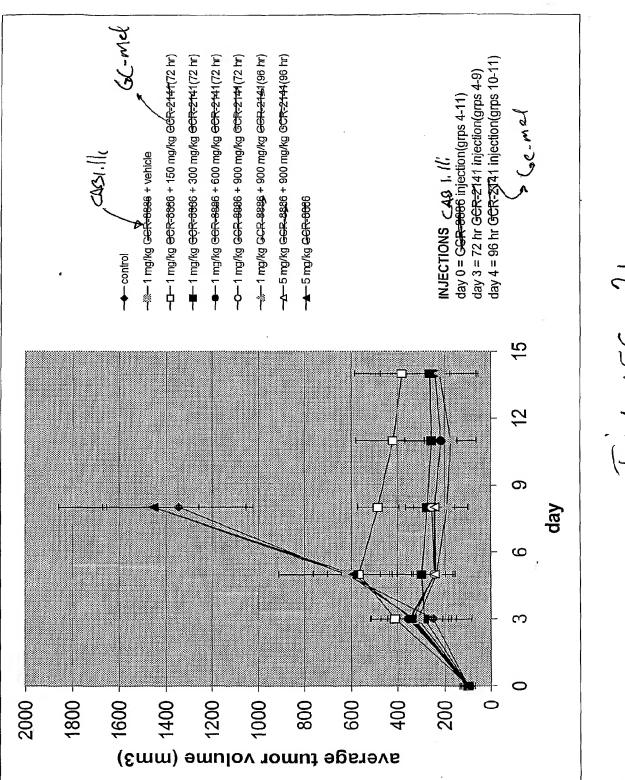
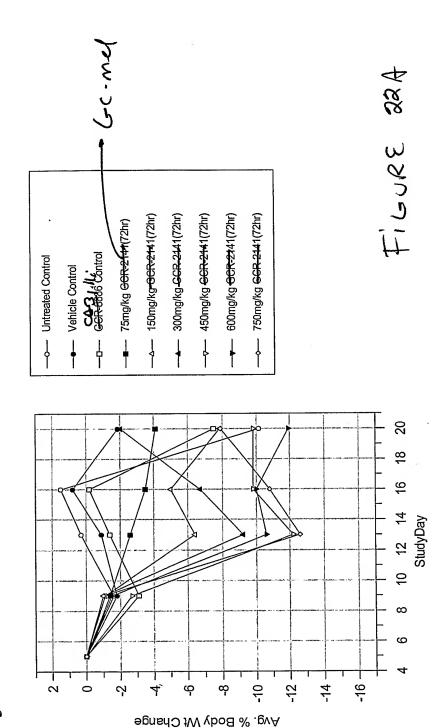


FIG 19B

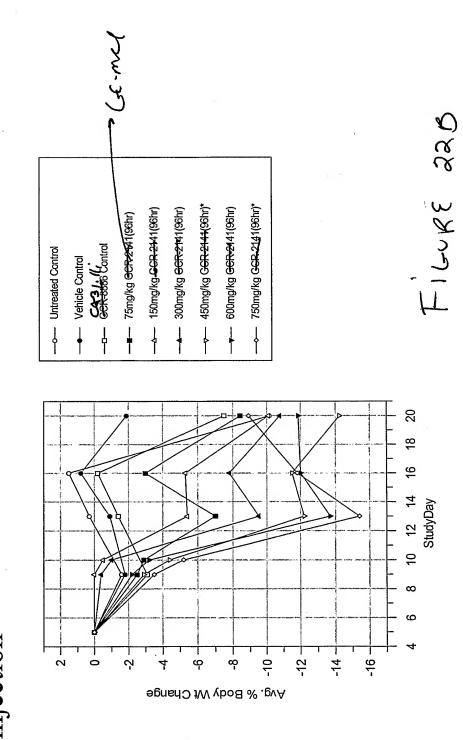


FILLUTE 21

(5C - Me)e 04-105 — Avg. % Body Wt loss — GGR-2141 injection 72 hrs (Study Day 9) post GCR-8886 injection

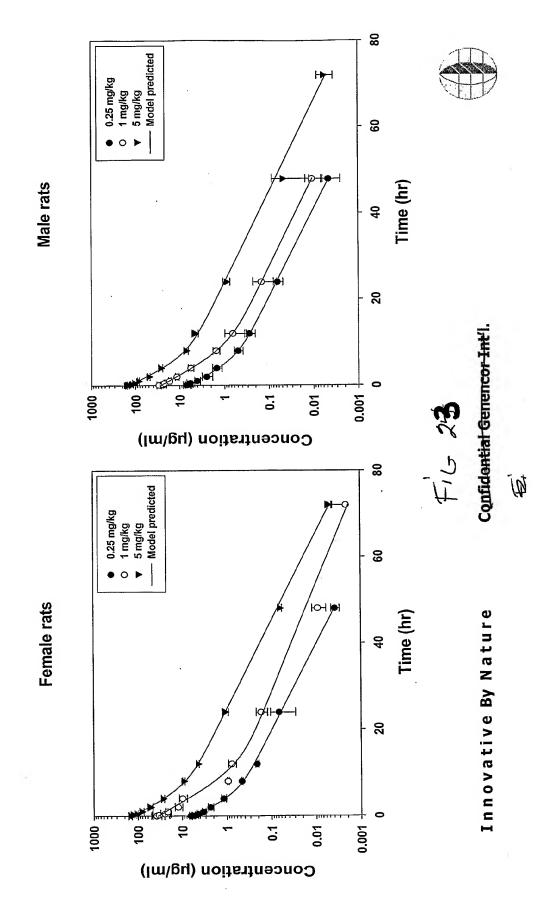


04-105 - Avg. % Body Wt loss - GCR-2141 injection 96 hrs (Study Day 10) post GCR-8886 C42 1:11/ injection



# CABRILL: Plasma GCR-8886 concentration-time profile in rats

Results

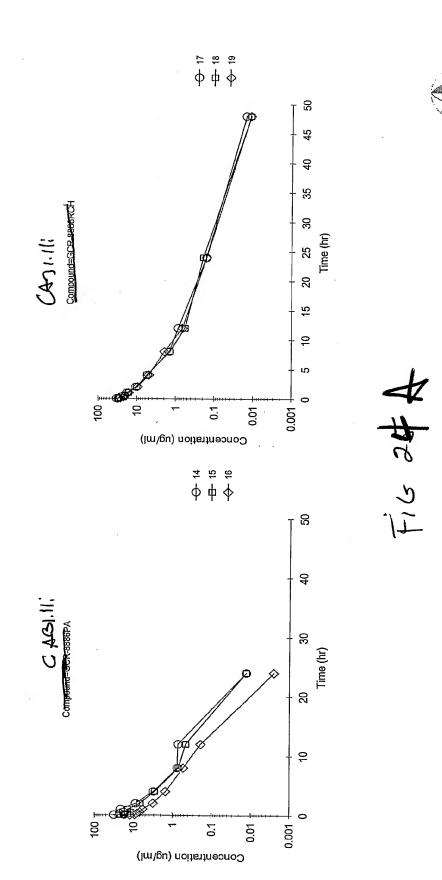


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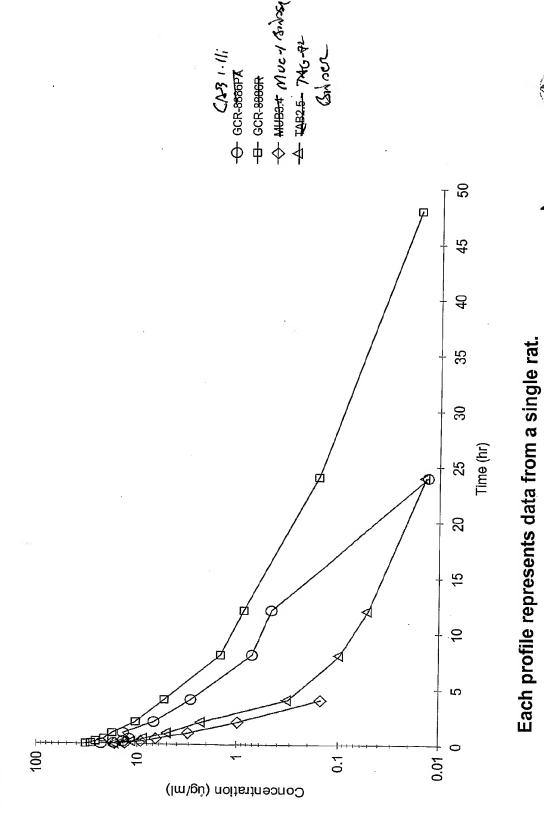
Innovative By Nature

# Plasma GCR-8886 concentration-time profiles in rats

Results



Plasma concentration-time profiles in rats Results



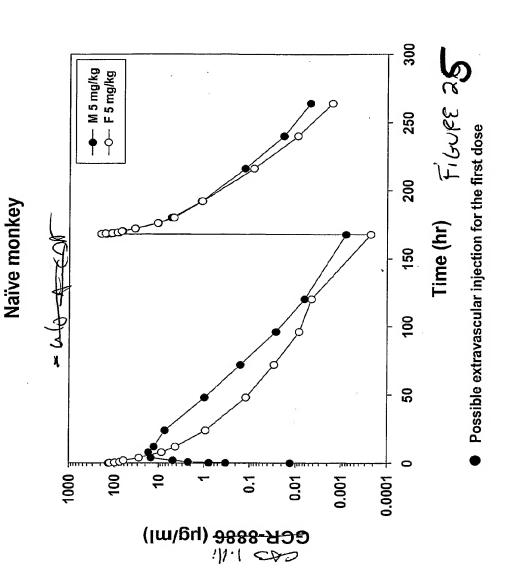
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GCR-8886 concentration-time profiles following 2 weekly doses



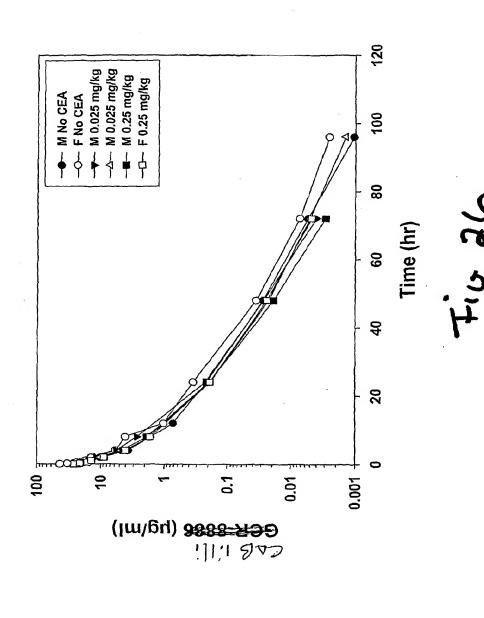


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Results

CA(S |.||; GCR=8886 (1 mg/kg)



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